

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Baumgartner, James W.  
Farrah, Theresa M.  
Foster, Donald C.  
Grant, Frank J.  
O'Hara, Patrick J.

(ii) TITLE OF INVENTION: Testis-Specific Receptor

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.  
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(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Parker, Gary E.  
(B) REGISTRATION NUMBER: 31,648  
(C) REFERENCE/DOCKET NUMBER: 95-33

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 49..1191

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCCCCGCC	GGGAGAGAGG	CAATATCAAG	GTTTAAATC	TCGGAGAA	ATG	GCT	TTC	57								
					Met	Ala	Phe									
							1									
GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA								105								
Val	Cys	Leu	Ala	Ile	Gly	Cys	Leu	Tyr	Thr	Phe	Leu	Ile	Ser	Thr	Thr	
5				10					15							
TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT								153								
Phe	Gly	Cys	Thr	Ser	Ser	Ser	Asp	Thr	Glu	Ile	Lys	Val	Asn	Pro	Pro	
20				25				30			35					
CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG								201								
Gln	Asp	Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Tyr	Leu	
				40			45			50						
CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG								249								
Gln	Trp	Gln	Pro	Pro	Leu	Ser	Leu	Asp	His	Phe	Lys	Glu	Cys	Thr	Val	
				55			60			65						
GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC								297								
Glu	Tyr	Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Gly	Ser	Glu	Thr	Trp	Lys	Thr	
				70			75			80						
ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG								345								
Ile	Ile	Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	
				85			90			95						

GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn 100 105 110 115	393
GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser 120 125 130	441
CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr 135 140 145	489
TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val 150 155 160	537
CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp 165 170 175	585
CAT GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile 180 185 190 195	633
GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr 200 205 210	681
ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr 215 220 225	729
TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr 230 235 240	777
CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser 245 250 255	825
ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu 260 265 270 275	873

ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu 280 285 290	921
ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val 295 300 305	969
GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser 310 315 320	1017
GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys 325 330 335	1065
ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val 340 345 350 355	1113
ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys 360 365 370	1161
ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT CCATATCAAG Met Ile Pro Glu Phe Phe Cys Asp Thr 375 380	1208
AGACATGGTA TTGACTCAAC AGTTTCCAGT CATGGCCAAA TGTTCAATAT GAGTCTCAAT	1268
AAACTGAATT TTTCTTGCAG A	1289

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile  
1 5 10 15

Ser Thr Thr Phe Gly Cys Thr Ser Ser Asp Thr Glu Ile Lys Val  
20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu  
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr  
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
165 170 175

Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly  
180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys  
195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg  
210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
225 230 235 240

Pro	Val	Tyr	Leu	Thr	Phe	Thr	Arg	Glu	Ser	Ser	Cys	Glu	Ile	Lys	Leu
														255	
245								250							
Lys	Trp	Ser	Ile	Pro	Leu	Gly	Pro	Ile	Pro	Ala	Arg	Cys	Phe	Asp	Tyr
														270	
260								265							
Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr	Leu	Val	Thr	Ala	Thr	Val
														285	
275								280							
Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr	Asn	Glu	Thr	Arg	Gln	Leu
														300	
290							295								
Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly
														320	
305					310					315					
Ile	Trp	Ser	Glu	Trp	Ser	Asp	Lys	Gln	Cys	Trp	Glu	Gly	Glu	Asp	Leu
														335	
325								330							
Ser	Lys	Lys	Thr	Leu	Leu	Arg	Phe	Trp	Leu	Pro	Phe	Gly	Phe	Ile	Leu
														350	
340								345							
Ile	Leu	Val	Ile	Phe	Val	Thr	Gly	Leu	Leu	Leu	Arg	Lys	Pro	Asn	Thr
														365	
355								360							
Tyr	Pro	Lys	Met	Ile	Pro	Glu	Phe	Phe	Cys	Asp	Thr				
														380	
370								375							

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 10..1152

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCCGCC	ATG GCT TTC GTT TGC TTG GCT ATC GGA TGC TTA TAT ACC	48
	Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr	
1	5	10
TTT CTG ATA AGC ACA ACA TTT GGC TGT ACT TCA TCT TCA GAC ACC GAG	96	
Phe Leu Ile Ser Thr Thr Phe Gly Cys Thr Ser Ser Asp Thr Glu		
15	20	25
ATA AAA GTT AAC CCT CCT CAG GAT TTT GAG ATA GTG GAT CCC GGA TAC	144	
Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr		
30	35	45
TTA GGT TAT CTC TAT TTG CAA TGG CAA CCC CCA CTG TCT CTG GAT CAT	192	
Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His		
50	55	60
TTT AAG GAA TAC ACA GTG GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT	240	
Phe Lys Glu Tyr Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly		
65	70	75
AGT GAA ACA TGG AAG ACC ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT	288	
Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp		
80	85	90
GGG TTT GAT CTT AAC AAG GGC ATT GAA GCG AAG ATA CAC ACG CTT TTA	336	
Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu		
95	100	105
CCA TGG CAA TGC ACA AAT GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA	384	
Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu		
110	115	120
ACT ACT TAT TGG ATA TCA CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG	432	
Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln		
130	135	140
GAT ATG GAT TGC GTA TAT TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG	480	
Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp		
145	150	155
AAA CCT GGC ATA GGT GTA CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC	528	
Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr		
160	165	170

TGG TAT GAG GGC TTG GAT CTT GCA TTA CAG TGT GTT GAT TAC ATC AAG	576
Trp Tyr Glu Gly Leu Asp Leu Ala Leu Gln Cys Val Asp Tyr Ile Lys	
175 180 185	
GCT GAT GGA CAA AAT ATA GGA TGC AGA TTT CCC TAT TTG GAG GCA TCA	624
Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser	
190 195 200 205	
GAC TAT AAA GAT TTC TAT ATT TGT GTT AAT GGA TCA TCA GAG AAC AAG	672
Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys	
210 215 220	
CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA	720
Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys	
225 230 235	
CCT TTG CCG CCA GTC TAT CTT ACT TTT ACT CGG GAG AGT TCA TGT GAA	768
Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu	
240 245 250	
ATT AAG CTG AAA TGG GGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT	816
Ile Lys Leu Lys Trp Gly Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys	
255 260 265	
TTT GAT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT	864
Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr	
270 275 280 285	
GCT ACA GTT GAA AAT GAA ACA TAC ACC TTG AAA ACA ACA AAT GAA ACC	912
Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr	
290 295 300	
CGA CAA TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA	960
Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser	
305 310 315	
GAT GAC GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGC TGG GAA GGT	1008
Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly	
320 325 330	
GAA GAC CTA TCG AAG AAA ACT TTG CTA CGT TTC TGG CTA CCA TTT GGT	1056
Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly	
335 340 345	

TTC ATC TTA ATA TTA GTT ATA TTT GTA ACC GGT CTG CTT TTG CGT AAG 1104  
 Phe Ile Leu Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys  
 350 355 360 365

CCA AAC ACC TAC CCA AAA ATG ATT CCA GAA TTT TTC TGT GAT ACA TGAAGACTTT  
 1159  
 Pro Asn Thr Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr  
 370 375 380

CCTCTAGA 1167

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile  
 1 5 10 15

Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val  
 20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
 35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu  
 50 55 60

Tyr Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
 65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
 85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
 100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr  
 115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
 130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
 145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
 165 170 175

Gly Leu Asp Leu Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly  
 180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys  
 195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg  
 210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
 225 230 235 240

Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu  
 245 250 255

Lys Trp Gly Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr  
 260 265 270

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val  
 275 280 285

Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu  
 290 295 300

Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly  
 305 310 315 320

Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu  
 325 330 335

Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu  
 340 345 350

Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr  
 355 360 365

Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Trp Ser Xaa Trp Ser  
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 11..1126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTTGGAGAA ATG GCT TTC GTC TAC TTG GCT ATC AGA TGC TTA TGT ACC  
 Met Ala Phe Val Tyr Leu Ala Ile Arg Cys Leu Cys Thr  
 1 5 10

TTT CTG ATA AGC ACA ACA TTC GGC TAT ACT TCA ACT TCA GAC ACC GAG Phe Leu Ile Ser Thr Thr Phe Gly Tyr Thr Ser Thr Ser Asp Thr Glu 15 20 25	97
ATA AAA GTT AAC CCA CCT CAG GAT TTT GAG ATA GTG GAT CCC GGA TAT Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr 30 35 40 45	145
TTA GGT TAT CTC TAT TTG CAA TGG CAA CCC CCA CTG TCT CTG GAT AAT Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp Asn 50 55 60	193
TTT AAG GAA TGC ACA GTG GAA TAT GAA CTA AAA TAC CGA AAC ATT GGT Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly 65 70 75	241
AGT GAA ACA TGG ACG ACC ATC ATT ACT AAG AAT CTA CAT TAC AAA GAT Ser Glu Thr Trp Thr Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp 80 85 90	289
GGG TTT GAT CTT AAC AAG GGC ATT GAA GCG AAG ATA CAC ACA CTT TTA Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu 95 100 105	337
CCA TGG CAA TGC ACA AAT GGA TCA GAA GTT CAA AGT TCC TGG GCA GAA Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu 110 115 120 125	385
GCT ACT TAT TGG ATA TCG CCA CAA GGA ATT CCA GAA ACT AAA GTT CAG Ala Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln 130 135 140	433
GAT ATG GAT TGT GTA TAT TAC AAT TGG CAA TAT TTA CTC TGT TCT TGG Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp 145 150 155	481
AAA CCT GGC ATA GGT GTA CTT CTT GAT ACC AAT TAC AAC TTG TTT TAC Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr 160 165 170	529
TGG TAT GAG GGC TTG GAT CGT GCA TTA CAG TGT GTT GAT TAC ATC AAG Trp Tyr Glu Gly Leu Asp Arg Ala Leu Gln Cys Val Asp Tyr Ile Lys 175 180 185	577

GTT GAT GGA CAA AAT ATT GGA TGC AGA TTT CCC TAT TTG GAG TCA TCA Val Asp Gly Glu Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser 190 195 200 205	625
GAC TAT AAA GAT TTC TAC ATT TGT GTT AAT GGA TCA TCA GAA ACC AAG Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Thr Lys 210 215 220	673
CCT ATC AGA TCC AGT TAT TTC ACT TTT CAG CTT CAA AAT ATA GTT AAA Pro Ile Arg Ser Ser Tyr Phe Thr Phe Glu Leu Glu Asn Ile Val Lys 225 230 235	721
CCT TTG CCA CCA GTC TGT CTT ACT TGT ACT CAG GAG AGT TTA TAT GAA Pro Leu Pro Pro Val Cys Leu Thr Cys Thr Glu Ser Leu Tyr Glu 240 245 250	769
ATT AAG CTG AAA TGG AGC ATA CCT TTG GGA CCT ATT CCA GCA AGG TGT Ile Lys Leu Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys 255 260 265	817
TTT GTT TAT GAA ATT GAG ATC AGA GAA GAT GAT ACT ACC TTG GTG ACT Phe Val Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr 270 275 280 285	865
ACC ACA GTT GAA AAT GAA ACG TAC ACC TTG AAA ATA ACA AAT GAA ACC Thr Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Ile Thr Asn Glu Thr 290 295 300	913
CGA CAG TTA TGC TTT GTA GTA AGA AGC AAA GTG AAT ATT TAT TGC TCA Arg Glu Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser 305 310 315	961
GAT GAT GGA ATT TGG AGT GAG TGG AGT GAT AAA CAA TGT TGG GAA GTT Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Glu Cys Trp Glu Val 320 325 330	1009
GAA GAA CTA TTG AAG AAA ACT TTG CTA CTT TTC TTG TTA CCA TTT GGT Glu Glu Leu Leu Lys Lys Thr Leu Leu Leu Phe Leu Leu Pro Phe Gly 335 340 345	1057
TTC ATA TTA ATA TTA GTT ATA TTT GTA ACC GGT CTG CTT TTG TGT AAG Phe Ile Leu Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Cys Lys 350 355 360 365	1105
AGA GAC AGC TAC CCG AAA ATG	1126

Arg Asp Ser Tyr Pro Lys Met  
370

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Phe Val Tyr Leu Ala Ile Arg Cys Leu Cys Thr Phe Leu Ile  
1 5 10 15

Ser Thr Thr Phe Gly Tyr Thr Ser Thr Ser Asp Thr Glu Ile Lys Val  
20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp Asn Phe Lys Glu  
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr  
65 70 75 80

Trp Thr Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln  
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Ala Thr Tyr  
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp  
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly  
145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu  
 165 170 175  
 Gly Leu Asp Arg Ala Leu Gln Cys Val Asp Tyr Ile Lys Val Asp Gly  
 180 185 190  
 Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys  
 195 200 205  
 Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Thr Lys Pro Ile Arg  
 210 215 220  
 Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro  
 225 230 235 240  
 Pro Val Cys Leu Thr Cys Thr Gln Glu Ser Leu Tyr Glu Ile Lys Leu  
 245 250 255  
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Val Tyr  
 260 265 270  
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Thr Thr Val  
 275 280 285  
 Glu Asn Glu Thr Tyr Thr Leu Lys Ile Thr Asn Glu Thr Arg Gln Leu  
 290 295 300  
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly  
 305 310 315 320  
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Val Glu Glu Leu  
 325 330 335  
 Leu Lys Lys Thr Leu Leu Leu Phe Leu Leu Pro Phe Gly Phe Ile Leu  
 340 345 350  
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Cys Lys Arg Asp Ser  
 355 360 365  
 Tyr Pro Lys Met  
 370

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG9801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGGTCCTTCC CATGTTTCAC TACCA

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG9941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTCGGTATT TTAGTTCATA TTCCA

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG9803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGAATTGG AGTGAGTGG A GTGAT

25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGAAGACCTA TCGAAGAAAA CTTTG

25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGCTTTCG TTTGCTTGGC TATCG

25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCTTGATAT GGAAAGTCTT CATGTATC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: AP1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: AP2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCTGATAGGC TTGTTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATAGCCAAGC AAACGAAAGC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCTGGCATA GGTGTACTTC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG9919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTGCCGCCAG TCTATCTTAC

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG10317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGGGGGTCTA GAGGAAAGTC TTCAATGTATC ACAG

34

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG10319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGGGGCTGG AGCTCGGAGA AATGGCTTTC GTT

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCCCCACTG TCTCTGGATC ATTTT

25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACCTTCCCA GCATTGTTTA TCACT

25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG10320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGGGGGAGAT CTTCAGACAC CGAGATAAAA GTT

33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG10318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGGGGGCTCG AGTTTCTTCG ATAGGTCTTC ACC

33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: ZG9882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTACTCTGTT CTTGGAAACC TGG

23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG10082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACTCTGTTCT TGGAAACCTG G

21

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (B) CLONE: ZG10083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAATGAAACA TACACCTTGA AAAC

24

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCATTGTTA TCACTCCACT C

21

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG9881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTCACTTTGC TTCTTACTAC AAA

23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACTAGCAGA TCTGGGCTCT TTCTTCGATA GGTCTTCAC

39

## (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10314

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCGTGATTCT CTGGTCGGTG

20

## (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(B) CLONE: ZG10315

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGATTGCTT TGGCGGTGAG

20